

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 17, 2001, 21:12:49 ; Search time 73.55 Seconds
(without alignments)
922,684 Million cell updates/sec.

Title: US-09-456-306-2
Perfect score: 2885
Sequence: 1 MAHSVAEQLIDTLEAGCVKR.....CGVGAMIDLARSINRIPTP 579

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_15:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organella:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1713	57.4	580	2	Q9ZBT3 streptomyc
2	855	28.6	574	2	P96591 bacillus su
3	693.5	23.2	600	2	Q9L147 streptomyc
4	637	21.3	553	1	Q26576 methanobact
5	616.5	20.7	587	1	Q918J0 methanococc
6	576	19.3	577	1	Q27493 synchocyst
7	567	19.0	621	2	P73913 methanobact
8	566.5	19.0	599	1	Q08353 methanococc
9	549	18.4	585	8	Q19929 cyanidium c
10	546	18.3	612	2	Q59950 spiliuina p
11	533.5	17.9	583	2	Q66739 aquilex aeo
12	536	17.6	548	2	Q916T2 salmonella
13	513	17.2	552	1	Q28554 archaeoglob
14	508	17.0	613	2	Q92567 streptomyc
15	502.5	16.8	584	2	Q9W218 thermocoga
16	498	16.7	591	2	Q9ZF24 streptococ
17	497	16.6	575	1	Q28180 archaeoglob
18	496	16.6	587	8	Q63181 porphyridiu
19	490.5	16.4	548	2	Q9KVV7 vibrio chol

20	490	16.4	583	2	Q9PCG0 xylella fas
21	486	16.3	562	1	Q9U210 pyrococcus
22	482.5	16.2	681	10	Q22578 volvox cart
23	480	16.1	599	10	Q05767 brassica na
24	475.5	15.9	561	2	P97113 leuconostoc
25	466.5	15.6	617	2	Q59816 streptomyc
26	461.5	15.5	572	1	Q9UWY1 sulfolobus
27	461.5	15.5	681	10	Q49210 volvox cart
28	461	15.4	594	2	Q45396 corynebacte
29	460	15.4	683	10	Q49229 chlamydomon
30	457	15.3	683	10	Q22547 chlamydomon
31	451	15.1	638	10	Q41768 zea mays (m
32	450.5	15.1	666	10	Q9ZSU3 bassia scop
33	450	15.1	659	10	Q42767 gossypium h
34	447.5	15.0	601	2	Q59272 caulobacter
35	443	14.8	659	10	Q42768 gossypium h
36	442	14.8	638	10	Q41769 zea mays (m
37	438	14.7	648	10	Q41717 xanthium sp
38	437	14.6	648	10	Q41716 xanthium sp
39	435	14.6	665	10	Q38795 amarantus
40	434.5	14.6	561	2	P94783 citrobacter
41	429	14.4	575	2	Q9JY10 neisseria m
42	427.5	14.3	573	2	Q9K990 vibrio chol
43	426.5	14.3	563	2	Q68497 clostridium
44	425	14.2	575	2	Q9JY11 neisseria m
45	418.5	14.0	524	1	Q27639 methanobact

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	580 AA.
ID	Q9ZBT3			
AC	Q9ZBT3			
DT	01-MAY-1999 (TREMBLrel. 10, Created)			
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)			
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)			
DE	PRIVVATE DEHYDROGENASE.			
GN	SC1A9.19.			
OS	Streptomyces coelicolor.			
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;			
OC	Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.			
OX	NCBI_TaxID=1902;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-A3(2):			
RA	Saunders D.C., Harris D.;			
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-A3(2):			
RA	Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;			
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=9700351; PubMed=8843436;			
RA	Redenbach M., Kleser H.M., Denapalte D., Eichner A., Cullum J.,			
RA	Kinasli H., Hopwood D.A.;			
RT	"A set of ordered cosmids and a detailed genetic and physical map for			
RT	the 8 Mb streptomyces coelicolor A3(2) chromosome."			
RL	Mol. Microbiol. 21:77-96(1996).			
EMBL	AL034446; CA22289.1; -.			
DR	INTERPRO: IPR000399; -.			
DR	PFAM: PF00205; TTP_enzymes; 1.			
KW	Pyruvate.			
SO	SEQUENCE 580 AA; 62503 MW; E4708ED5A1C8588 CRC64;			

Query Match 57.4% Score 1713; DB 2; Length 580;
Best Local Similarity 57.5%; Pred. No. 5,6e-109;
Matches 331; Conservative 92; Mismatches 149; Indels 4; Gaps 4;


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Db 411 GCGILPGAIASLSEPEAOALAVCGDGFSAWMODLPYAVYKYLPTVILNNENLGMTEY 470
OY 472 EMLVEGQPEGTDEHEENFAEIAAAGIKSVRTIDPKKVEQALAEALAYGPLYIDVTD 531
Db 471 EGVAVKGNIDVYTLQNVADVAAAFESCGAKIKYTKAEELPAFHAEALHSDQPVYVDWIG 530
OY 532 PNAISIPPTITWQVGFSAKATRTVEGGVGAMIDLARS 571
Db 531 -NEPPLPGKITTYGAKGFSKYMLKNFEENQKFMPSLKKS 569

RESULT 3
OY 09L147 PRELIMINARY: PRT: 600 AA.
AC 09L147:
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE PUTATIVE PYRUVATE DEHYDROGENASE (PYRUVATE OXIDASE).
GN SC6D11.08.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxId=1902;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Seeger K.J., Harris D.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN 12
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN 13
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Redenbach M., Kleiser H.M., Denapalte D., Eichner A., Cullum J.,
RA Klinosh H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome."
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL: AL158061; CAB76331.1; -.
KM Pyruvate.
SQ SEQUENCE 600 AA: 65282 MW: A5DDDA8382B7D90F CRC64;

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Db 305 MIGIRYPMDAHLVSDSRETLRALIPMLQRRKKDRGMREKIEK-DVREHMDLCDRR---AGE 360
OY 356 HV--PIHEEVASTLNLAQKDAVFYVDTGMCNNVHARYIENPEGTDDPFGSPFHGTMAN 413
Db 361 HEGKTIIPQAVVAEELSLARLPDDVYLTLDSSGTTMMARHLL---LRDGMQASLSCTLAT 416
OY 414 ---ALPHAIAQSVDRNRQVYIACMGDGLGML-LGELLTVKLH-----QLPLKAVFNN 463
Db 417 MGSTPYAIAARFAYRPRPIAIFGDGAFQMGNGENHITYKRYIDRLSGSRPLIFCYFNN 476
OY 464 SSLGMVKLEM-LVEGQPEF--GTDEEENFAEIAAAGIKSVRTIDPKKVEQALAEALAY 520
Db 477 QDLNQVTEORAMAGDKRYPGSODIPDYPYAAVALLGLKGIYCDDPKKVGAAMDALISA 536
OY 521 PGPLYIDVTDPNALSTPTITWQVGFSAK 553
Db 537 GRPVLEFQVDAETAPIPIHMKRKAIAKAA 569

RESULT 4
OY 026576 PRELIMINARY: PRT: 553 AA.
AC 026576:
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE PYRUVATE DEHYDROGENASE / ACETOLACTATE SYNTHASE.
GN MTH476.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanobacterium.
OX NCBI_TaxId=2166;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN-DELTA H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A.;
RA Aldridge T., Shahrzadeh R., Blakey D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Potlher B., Qiu D.,
RA Spadafora R., Vicare A., Bush D., Sifer H., Patwell J., Gibson R.,
RA Jiwani N., Caruso A., Wang Y., Mierzbowski J., Prabakar S.,
RA McDougall S., Shiner G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Nollan J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics."
RL J. Bacteriol. 179:7135-7155(1997).
DR EMBL: AE000832; AAB84982.1; -.
DR HSSP: P00269; 1RB9.
DR INTERPRO: IPR001399; -.
DR INTERPRO: IPR001052; -.
DR INTERPRO: IPR003252; -.
DR PFAM: PF00205; TTP_glycylases; 2.
DR PFAM: PF00301; rubredoxin; 1.
DR PRODOM: PD001610; -. 1.
KM Pyruvate.
SQ SEQUENCE 553 AA: 60506 MW: 17B385DE4AEC938 CRC64;

Query Match 21.3%; Score 637; DB 1; Length 553;
Best Local Similarity 30.4%; Pred. No. 2e-35;
Matches 164; Conservative 95; Mismatches 224; Indels 56; Gaps 6;

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Db 175 VYNNMLVSPDEAAELAREAVKHAILERGVSHVDPEDV-----QTMECTAPVK 222
OY 184 -----VPPDPEAAALVEAINNAKSVTLFCGAGYKNAPOYLEAEIKSPIGIA 233
Db 223 PLRGMAEAAVPPRNRRLAAADLINRAERPIIAGFGALEAADSVELAEIRIGAIVST 282
OY 234 LGKQVIOHENEFEVSGSLGAGYCADASNEADLLILGTPEPPYSDLPKNNVQVDIN 293
Db 283 ERKKGIVNDYDPLYLSCGSLSAALAEVRAKADLLLVGSSFDLTRIPRRTLOVDID 342
OY 294 GAHIGRTTVKYPVGVDAATIENTILPHVKEKTRSDRLMLKAHKKLSVVEITYTHV 353
Db 343 PMVVARHNEVEGRLTGRSSLIYQELISWBEKRGPIYLAELGELRDEMGLLESEADPSL 402
OY 354 EKHPVTHPEVYASILNELADKDAVFTVDTGMCNVAIRIENPEGTRDVGSRHGTMAN 413
Db 403 R---PIRPQYIISVLNRELDDDAITILDGENGWFGNRFO--MKSTRGSPFOYTWGSMGF 458
OY 414 ALPHAIAGOSVDRNRQIVAMCGDGLGMLLGELLIVKHLQPLKAVFNNSSILGWKLEM 473
Db 459 GLPAAIAQLEFPDROVCL-----NNRNLAIMIQEO 490
OY 474 LVEGDEFGTDEEVENFAETAAAGIKSVRIIDPKRVREQLAEALAYEGPVLIDVTP 532
Db 491 RVGCFVWQTELODCDFAGFACNCGRGLRVDDPGLEDSVREALGTGDPVLVIDETDP 549

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RESULT 5
OY8J0 PRELIMINARY; PRT; 587 AA.
ID 09Y8J0;
AC 09Y8J0;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ACETOHYDROXYACID SYNTHASE LARGE SUBUNIT (EC 4.1.3.18).
GN ILVB.
OS Methanococcus maripaludis.
OC Archaea: Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=39152;
RN [1]
RP SEQUENCE FROM N.A.
RA Gardner W.L., Whitman W.B.;
RC STRAIN=JJ;
RT "Development of integrative and shuttle vectors for Methanococcus
maripaludis";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
DR EMBL: AF118061; AAD28737.1; -.
DR HSSP: P06169; LPVD.
DR INTERPRO: IPR000399; -.
DR PFAM: PF00205; TPP_enzymes; 1.
DR PROSITE: PS00187; TPP_ENZYMES; 1.
KW Lyase; Flavo-protein; Thiamine pyrophosphate.
SQ SEQUENCE 587 AA: 63837 MW; A31D942AA71FE440 CRC64;

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Query Match 20.7%; Score 616.5; DB 1; Length 587;
Best Local Similarity 29.9%; Pred. No. 5,5e-34;
Matches 167; Conservative 110; Mismatches 250; Indels 31; Gaps 13;
OY 6 AEOLIDLEAGVKRYIGLVGDSLNPIVDVAVROSIDEMVHVRNEAFAAGAESLTIGE 65
Db 4 AEAAMKALEENKVKVLEFGYGGQLLPYDALYQSDFLHILTRHQAANAHAADGVARASGD 63
OY 66 LAVCAASGPGCNTHLIGLYDSHRNGAKVLAISHIPSAOIGSTFEOETHPELIFKESG 125
Db 64 VGVCAVATSGGATNVLGVATAHADSSPVVALTGOVPTKLIGNDAFOEIDALGTFMTK 123
OY 126 YCEVNVNGDEGERTLHIAISTAGK-GVSVVYIPGDIAMEDAGDGY---SNSTISSGT 181
Db 124 HNFQIOKTSPIKIFERRAFIAKTGRGAVAVHVDLPKVDVDDLDLEKYPPIPAETINLGK 183

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OY 182 PVFPDPEAAALVEAINNAKSVTLFCGAGYK--NARAQVLEAEIKSPIGHALGKQY 239
Db 184 PTKPHPIQIKAAELMKIAQRPVLIAGGVOIADNATPELLKLSYQIIPCTTLMGKV 243
OY 240 IOHENEFEVSGSLGAGYCADASNEADLLILGTDF-----PISDLPKPDNVAQVDIN 293
Db 244 FPEEHPILSGWGMHGTQASNSVYESDVLIAIGCFSDRITRGDLSFAPNPKVNIHID 303
OY 294 GAHIGRTTVKYPVGVDAATIENTILPHV--KEKTRSDRLMLKAHKKLSVVEITYTH 351
Db 304 PAEIGKNVGVDPITVGDAAKAILKILHMKKEVKNKTEMENYVKLOKKSPPWEEF--- 360
OY 352 NVEKHVPDHE-YVASILNELADKD-----AVFTVDTGMCNVAIRIENPEGTRDVG 405
Db 361 ---DNTPIKPKQVINEEMAALEVEPDGLNTVLTLDVGQNMWMMHYPT--SAPKSFSS 416
OY 406 FRHGTMANALPHAIAGOSVDRNRQIVAMCGDGLGMLLGELLIVKHLQPLKAVFNNSS 465
Db 417 GGQGTWGFEGFPAAIGAKFAPDANVIAVYDGGFLMNSQELATVIEYELPIVTVFDKRT 476
OY 466 LGMV-KLEMLVEGDEFGTD-HEEVNFAETAAAGIKSVRIIDPKRVREQLAEALAYEGP 523
Db 477 LGWVQWQNLTYGKKQCAVHLGETPDKLASYGIALRVKPEPDINEAFKTLANSKRP 536
OY 524 VLIDVTPDN-AL-STPP 539
Db 537 YLDDITIDPESEALHMYPP 554

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RESULT 6
ID 027493 PRELIMINARY; PRT; 577 AA.
AC 027493;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ACETOYLACTATE SYNTHASE, LARGE SUBUNIT.
GN MTH144.
OS Methanobacterium thermoautotrophicum.
OC Archaea: Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanobacterium.
OX NCBI_TaxID=2166;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.R., Doucette-Stamm L.A., Delonghery C., Lee H.-M., Dubois J.,
Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Sater H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pletrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
CC -1- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
DR EMBL: AE000905; AAB85919.1; -.
DR HSSP: P06169; LPVD.
DR INTERPRO: IPR000399; -.
DR PFAM: PF00205; TPP_enzymes; 1.
DR PROSITE: PS00187; TPP_ENZYMES; 1.
KW Flavo-protein; Lyase; Thiamine pyrophosphate.
SQ SEQUENCE 577 AA: 62674 MW; A9318489D2D77142 CRC64;

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Query Match 19.3%; Score 576; DB 1; Length 577;
Best Local Similarity 26.8%; Pred. No. 3,1e-31;
Matches 149; Conservative 117; Mismatches 267; Indels 24; Gaps 9;
OY 7 EOLIDLEAGVKRYIGLVGDSLNPIVDVAVROSIDEMVHVRNEAFAAGAESLTIGE 66
Db 8 QATIRSLDQADTVFVYEGQLLPYDKMLYDSEILHILVRHQAANAHAADGVARASGRV 67

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QY	67	AVCAASCPGNTUHLIOGLYDSHRGACVALLIASHPAOLGSGTFEPOTHELLFKBCSG	126
Db	68	GVCLATSPGATNLVTGLATATYMSAIVAIACQVPHLIGNAFQCEVDMIGITPTKH	127
QY	127	CEMVNGCEGGERILLHAIQSTMAK -GVSVVVIIPGDIADKEDAGDGYTNSSTISSGPPVF	185
Db	128	SFQSPDASEIPALVIRASPHIAKTRGPPVVIDLPKQIOEOEIME -EYDDELLEGRPNVK	186
QY	186	PDPPEAAALVAILNNAASVTLFCGAGV -KNARQVLELAELKISPLGHALGKQYIOHE	243
Db	187	CHPLQIKRAAMELIRRSKPVILAGCGVITISGASREIKELSDLIKAPVTTLLCKGSPED	246
QY	244	NPEFVGMSGLGACVADASNEADLLTLGCTDEP-----YSDFLPKDVAQVDINGAIH	297
Db	247	HPSAMGMLGIMGRVAVNLVYDECCCLLAVGCGCRSDRTGTVAEFAPNARIINHVIDPAEL	306
QY	298	GRRTTVKTPVYTGDAATIENTLPIVK -EKTDSFLDRLMKAHKRLSVSEVETYNHVK	355
Db	307	GKNVGDVPITVGDAARNVLRRLIAKLKRYEKRDQSOWLESYOKFR-----ADCMPRMSYD	359
QY	356	HVPYIPEVVASILNELDKDAVFVDVDMGNVNHARIENPECTRDPVGSFRIGTAMNL	415
Db	360	EVPLAKPQOVIKEISOVLDETVTTTVDYGQNMMAHFYTS -RAPKRFISSGGLTGTCFGE	418
QY	416	PHATGASVDNRNOVIAACGGCGGLMGLGELLTVKHLQDLKAVFNSSLAGWKLEMLV	475
Db	419	PALGAKAVLDPDSVAVVAVCGGCGFLAVGCDLATIREVDIPVICINDIRHLGVAQOMRL	478
QY	476	EGQPEFGTCH--EEVNAELIAAAGTISVITTPPKKVRQEDALARALVPGVULDIYTDGN	533
Db	479	FYDERMSHTHLCEVPDPVKLAESFGVEAKRIIEPGETSEALSRAINSGEFALDVIDDPD	538
QY	534	AL--SIPPTITWEQVMG	548
Db	539	EILPMVPPGCGCLTEIVG	555
RESULT	7		
P73913	ID	P73913	PRELIMINARY; PRT; 621 AA.
AC	P73913;		
DT	01-FEB-1997 (TREMBLrel. 02, Created)		
DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)		
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)		
DE	ACETOHYDROXY ACID SYNTHASE.		
GN	ILVg.		
OS	Synechocystis sp. (strain PCC 6803).		
OC	Bacteria; Cyanobacteria; Chroococcales; Synechocystis.		
OX	NCBI_Taxid=1148;		
NN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=97061201; PubMed=8905231;		
RA	Kaneke T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,		
RA	Myajima N., Hirosewa M., Sugitara M., Sasamoto S., Kimura T.,		
RA	Hosouchi T., Matsuno A., Muraiki A., Nakazaki N., Naruo K., Okumura S.		
RA	Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,		
RA	Tobata S.;		
RT	"Sequence analysis of the genome of the unicellular cyanobacterium		
RT	Synechocystis sp. strain PCC6803. II. Sequence determination of the		
RL	entire genome and assignment of potential protein-coding regions."		
RL	DNA Res. 3:109-136(1996).		
DR	EMBL: D90910: BAA17977.1: -		
DR	HSSP: P06169: 1PVD.		
DR	INTERPRO: IPR000399: -		
DR	PRAM: PF00205; TPP_enzymes; 1.		
QO	SEQUENCE 621 AA; 67730 MW; 1A1A6GC370AE9C34 CRC64;		

Query Match	19.0%;	Score 567;	DB 2;	Length 621;
Best Local Similarity	-27.4%;	Pred. No. 1.5e-30;		
Matches 164;	Conservative 113;	Mismatches 236;	Indels 86;	Gaps 18

QY	9	LIDLEAGVYRIRIGLVDSINPIYDAVRO----	SDIEWYVNRDEEAAFPAGAESILTG	64
Db	27	LMDSLKRGVYKHIGIRYBGGALLPIYDELYRE	MAGEIPIHILVNRDEGASNAADYARTG	86
QY	65	ELAVCAASGFGENTHIDGLYDSHNRGAKVLA	SHIPSAOIGSTFEO-----THPEI	110
Db	87	KVGCFCGTSGATMLYVGINAHLDSPVYVIT	GVGVGRAMIGDAFOEIDIFGITLPIV	140
QY	119	LFKESGCEVNVNGEGSERILHNAIGSTMAK-	GVSUVYVPGIAKE-----DAGDG	170
Db	147	-----KISUYVRSADMARIVTAEFIHLS	TSGRGVPLIDIPKDVGLSECEYILDPD-	199
QY	171	TYSNSTISSGTVYVPRDTEAAALVEATINNK	SVTLFCGAG--VKNRAOVLTAELAKKS	222
Db	200	-----VNPGRYPTUKGNPRQJNALLOLEQ	ARNPLLYGSGALANAHAOQOEFERQOL	255
QY	229	PIGHALGSKOYIOPENREPEVMSGILLYGAC	SVDAENSEADLLILGLTF-----PYSDFL	287
Db	256	PVTTLMGIGAFDENHPLSVGMILGNHGYA	NPAVSECDLLILANGARRDQVGTCKLDEFA	311
QY	283	PKDVAOYVDINGANIIGRTTYKYRVUGDAV	TENILPRYKE-----KTORSFLDRLM	333
Db	316	SRAKVINDIDIPRAEYGKRNARDVILGVB	RIHLEQLLORAELDYPTPIHTQAMLNR--	372
QY	336	KAHEKLISSVVEYETHNNEKIVPRINREVA--	STINELADK--DAVFTVDTGMCNVNNAH	397
Db	374	-----IDHMMTDPLOIOPRHXEDIAIOE	VVNHGROAPRAYTTDGOHOMMAO	423
QY	392	YIENEGTRDFVGSFRIGTMTANALPRHAIG	SAOSVDRNROYIAMSGDGLMILGELLTVKL	451
Db	424	PLNN--GRRRIISSAGLCTMGFCIRAMNGA	LVGVGDEVAICISDASOMYLOELGTIAQ	487
QY	452	HOLPLKAVVENSSIGMYK-----LEMI	VEGOREFGTDHEEVNFAETIAAAGI	495
Db	482	YDIOKVTIILNNGOGVRYOQOFTFEERY	SASNNMSGMP-----DINL--LCEAYGI	532
QY	500	KSVRTIDPKVVRBOELAEIAYRGVLLDIYV-	DPNML-STPIPTITMEOVNGFSKATR	555
Db	533	KGTVRRKREDDARPAIEALINRGVAVDVU	YVKKKQENCSYPTIAPRMSNMOKIGLEVPVR	591

RESULT	8			
008353				
ID	008353	PRELIMINARY;	PRT;	599 AA.
AC	008353;			
DT	01-JUL-1997 (TREMblrel, 04, Created)			
DT	01-JUL-1997 (TREMblrel, 04, Last sequence update)			
DT	01-MAY-2000 (TREMblrel, 13, Last annotation update)			
DE	ACTOXYDROXYACID SYNTHASE LARGE SUBUNIT (EC 4.1.3.18)			
DE	(ACTOLACTATE SYNTHASE).			
GN	ILVB.			
OS	Methanococcus aeolicus.			
OC	Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;			
OC	Methanococcus.			
OX	NCBI_TaxID=42879;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97254452; Pubmed=9099862;			
RA	Bowen T.L., Union J., Tumbula D.L., Whitman W.B.;			
RT	"Cloning and phylogenetic analysis of the genes encoding			
RT	acetoxydihydroxyacid synthase from the archaeon Methanococcus aeolicus.";			
RL	Gene 188:77-84(1997).			
CC	-1- CATALYTIC ACTIVITY: 2-ACETOLACTATE + CO(2) -> 2 PYRUVATE.			
CC	-1- COFACTOR: THIAMIN PYRROPHOSPHATE.			
CC	-1- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.			
DR	EMBL; U53458; AAB53488.1; -			
DR	INTERPRO; IPR000399; -			
DR	PFAM; PF00205; TPP_ENZYMES; 1.			
DR	PROSITE; PS00187; TPP_ENZYMES; 1.			
KW	LYASE; Flavoprotein; Thiamine pyrophosphate.			
SQ	SEQUENCE 599 AA: 65423 MW: 59630C57DEC0D62 CRC64;			

Query Match 19.0%, Score 566.5; DB 1; Length 599;
 Best Local Similarity 28.3%; Pred. No. 1.5e-30;
 Matches 161; Conservative 109; Mismatches 255; Indels 43; Gaps 15;

6 ABLDITLAEAGVRRIVGLVDSINPIYDAV---RQSDIEWVHNRDEAAFAAGAESLITG 65
 4 AEMAKLAEAEVVELFEGPGALLPEYDALHSDLIHLTRHEQAAAHAAAGVYARAGK 63
 QY LAVAACSCGPGNTHLIGLSDSHRNKAKVLAISHIPSAQISFTFOETHPELFEKCSG 125
 66 VGVCGTSGPGATNLVTAATAHSDSPVVALTGQVPTKLIGNDAFOELDGLFMPYTK 123
 Db 126 YCEMVNGSEEGEGRILHHAIOSTMAGK-GVSVVVIPIGDIADAGDGTG---SNSTISSGT 181
 124 HNFQIOKTCQIPELFRSAFELAQGRPGVHIDLPKVOELEDIDKHPIDISKVLGIN 183
 QY 182 PVFPPDPTEAALVLEAINNAKSVTLFCGAGV--KNARQVLELAKISPIGHALGKQY 239
 184 PTTIGHPRQIKAKLKILASAKRPILLAGGVLISGANBELKLVELLIPVCTTLMGKC 243
 QY 240 IOHENPFEVNGSGLLYGACVDASNEADLLILGTFD-----PYSDFLPKDNVAQVDIN 293
 244 ISENHPLALGMVGMHGTFRANVCLESVDLISIGCRFSDRTITGDKSPATNAKTIHID 303
 QY 294 GAHIGRRTTVKYPVTGDVAATENTILPHV-----KEKTRDFLDRMLK-AHERKLSS 344
 304 PAELIKNNVNDVPIVGDVAKLLIKEVIKQLDYIINKSKENDKENDKEMISQIENVNSLKKSS 363
 QY 345 V-VETVTHNVKHPVHIEHYASTINELAD-----KDAVFYVDGMCVNHARYIENEG 398
 364 IPVMDY-----DPIPKQKTKVKEMLAVIDLINKNITITTDGONOMMAHFKT-QT 417
 Db 399 TRDFVSGFRHGTMANALPHAIGASVDNRNOVIAMCGDGLMLGELLITVYKHLPLKA 458
 418 PRSFLSSGGLTGMGGEFSAIGAKAPDSKVICITGDSGGMNNOELGTTAETVPIYV 477
 QY 459 VFNNSISGMV-KLEMLVEGPE---FGTDEEVNFAEIAAAGIKSVRTDPKRVREQ 513
 478 CIFDKRTGLMYQWONLFFYGRKQCSVNEG---GAPDFIKLAEYGIKARIESPEINEA 534
 Db 514 LAELALPGVPLIDIVDP-NALS-IRP 539
 535 LKEALNCEPYLIDFALDPSALSMP 562

RESULT 9
 ID 019929 PRELIMINARY; PRT; 585 AA.
 AC 019929;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE ACETOHYDROXYACID SYNTHASE LARGE SUBUNIT.
 GN ILV.
 OS Cyanidium caldarium (Geldieria sulphuraria).
 OG Chloroplast.
 OC Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;
 OC Cyanidium.
 OX NCBI_Taxid=2771;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=RR1;
 RA Gloeckner G., Rosenthal A., Valentin K.;
 RL Submitted (sep-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
 DR EMBL: AF022186; AAB82660.1; -
 DR HSSP: P06169; IPVD.
 DR MENDEL: 23174; Cyaca; 1145; 23174.
 DR INTERPRO: IPR000399; -
 DR PFAM: PF00205; TPP_enzymes; 1.
 DR PROSITE: PS00187; TPP_ENZYMES; 1.
 DR Chloroplast; Flavoprotein; Lyase; Thiamine pyrophosphate.
 KW SEQUENCE 585 AA; 65123 MW; 1795558676011 CRC64;

Query Match 18.4%, Score 549; DB 8; Length 585;
 Best Local Similarity 27.3%; Pred. No. 2.2e-29;
 Matches 160; Conservative 112; Mismatches 247; Indels 68; Gaps 15;

9 LIDTLEAGVRRIVGLVDSINPIYDAV---RQSDIEWVHNRDEAAFAAGAESLITG 64
 16 LIDMLVKHKNVNIQYPCGALLPIYDELHYHEKKKLIKHYLRHQSAAHAAADYARATN 75
 Db 65 ELAVCAACSCGPNTHLIGLSDSHRNKAKVLAISHIPSAQISFTFOETHPELFEKCS 124
 76 EVGVCLATSGPGATNLVTAATAHSDSPVVALTGQVPTKLIGNDAFOELDGLFMPYTK 135
 QY 125 YCEMVNGSEEGEGRILHHAIOSTMAGK-GVSVVVIPIGDIADAGDGTG---SNSTISSGT 179
 136 KHSFVRDPRDITSTVSAFYISKHGRGAVLIDVPKGVGLEENYHYDYSIRDHKPTK 195
 QY 180 GTPVFPDPTEAALVLEAINNAKSVTLFCGAGVKNARQ--VLEAEKIKSPIGHALGK 237
 196 YRPIGPIRQIEKFKMLLESKQILYVGGAVMASRQHIELASTIKIPVTTLMGK 255
 QY 238 QYIOHENPFEVNGSGLLYGACVDASNEADLLILGTFD-----PYSDFLPKDNVAQVD 291
 256 GSFNEYNPLYLGMGMHGTAVANFAVSECDDLIALGARFDDRYTGKIDFACNAQVIHV 315
 QY 292 INGHIGRRTTVKYPVTGDVAATENTILPHYKERTDNRFLDRMLK-AHERKLSSVETVTH 351
 316 IDPAELIKNNRIPQALITSDIKTVLKEKLSKKEGNN--MDK-----NOTQAMHL 363
 Db 352 NVK-----HVP-----IHPEVASTINELADKDAVFYVDGMCVNHARYIENEGT 399
 364 RIKHWKREPLSTPHDSKLLPQEVINETSIOAK-AFAFDVGOHOMMAQFLKVGOG- 421
 QY 400 RDFVSGFRHGTMANALPHAIGASVDNRNOVIAMCGDGLMLGELLITVYKHLPLKA 459
 422 -KWLSSGGLTGMGGLPAIGATIANPDLLITGTCGASFOQNLQELGTIQAQYELDIK 480
 QY 460 VFNNSISGMVKT-----EMLVEGPEEGTDEEVNFAEIAAAGIKSVRTDP 507
 481 IINNOGQVNOQOAFYDQRYANSMNAKGPD-----FVQLANSVGIRGIRVTT 531
 Db 508 KKEVQALAEALPGVPLID--IVTDNAL-SIPPTTQEWGMSK 551
 532 KDLKSKIERITSTPGPLIDICIVATSENCYMPINAPGKSNQSMGLTK 578

RESULT 10
 ID 059950 PRELIMINARY; PRT; 612 AA.
 AC 059950;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE ACETOHYDROXY ACID SYNTHASE (EC 4.1.3.18) (ACETOLACTATE SYNTHASE)
 GN ILV.
 OS Spirulina platensis.
 OC Bacteria; Cyanobacteria; Oscillatoriales; Spirulina.
 OX NCBI_Taxid=1156;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=92381487; PubMed=1512571;
 RA Milano A., de Rossi E., Zanatta E., Barbierato L., Ciferri O.,
 RA Ricciardi G.;
 RT "Molecular characterization of the genes encoding acetoaldehyde acid
 RT synthase in the cyanobacterium Spirulina platensis.";
 RL J. Gen. Microbiol. 138:1399-1408(1992).
 CC -1- CATALYTIC ACTIVITY: 2-ACETOACTATE + CO(2) = 2 PYRUVATE.
 CC -1- COFACTOR: THIAMIN PYROPHOSPHATE.
 DR EMBL: W5906; AAA26594.1; -
 DR HSSP: P06169; IPVD.
 DR INTERPRO: IPR000276; -

[illegible]

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DE ACETOGLUTARATE SYNTHASE, LARGE SUBUNIT (ILVB-1).
GN AF1720.
OS Archaeoglobus fulgidus.
OC Archaeae, Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC Archaeoglobus.
NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Kleck H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kervilavage A.R., Grahm D.E., Kyrides N.C.,
RA Flatschmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kikness E.F., Dougherty B.A., McKenney K.C., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.G., Glodet A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Colton M.D., Spriggs T., Artchak P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., DAndrea K.F., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370(1997).
CC -i- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
DR EMBL: AE000985; AAB89531.1; -.
DR HSSP: P37063; 1PCX.
DR TIGR: AF1720; -.
DR INTERPRO: IPR000399; -.
DR PFAM: PF00205; TPP_enzymes; 1.
DR PROSITE: PS00187; TPP_ENZYMES; 1.
KM Hypothetical protein; Flavoprotein; Lyase; Thiamine pyrophosphate.
SQ SEQUENCE 552 AA; 59974 MW; 6944132C525F8245 CRC64;

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Query Match	Similarity	17.2%	Score 513	DB 1	Length 552
Best Local	Similarity	26.7%	Pred. No. 5	9e-27	
Matches 153	Conservative	104	Mismatches 255	Indels 56	Gaps 13

DB 463 GWR-----OMOLEFYRENSATCIGCEKTCGEAIAKRGCAIGCMVKEPSEVDALKEAK 517
 QY 519 AVPGVLIDIVDPNA---LSIPPTTMEQVM 547
 DB 518 EVDAPVIVDFRDYQANVPMVPRGAALNEII 549

RESULT 14

Q92567 ID PRELIMINARY: PRT: 613 AA.
 AC 092567: 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
 DE ACETOLACTATE SYNTHASE.
 GN SC8D9.24.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomyetaceae; Streptomyces.
 OX NCBI_Taxid=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Murphy L., Harris D.;
 RL Submitted (Feb-1999) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (Feb-1999) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kleiser H.M., Denapalte D., Elchner A., Cullum J.,
 RA Khasht H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 DR Mol. Microbiol. 21:77-96(1996).
 DR EMBL: AL035569; CAB3588.1;
 DR INTERPRO: IPR000399;
 DR INTERPRO: IPR000847;
 DR PFAM: PF00205; TTP_enzymes; 1.
 DR PROSITE: PS00044; HTL_LYSR_FAMILY; UNKNOWN_1.
 DR PROSITE: PS00187; TTP_ENZYMES; UNKNOWN_1.
 SO SEQUENCE 613 AA: 65223 MW: 8P1378B37003429 CRC64;

Query Match 17.0%; Score 508; DB 2; Length 613;
 Best Local Similarity 27.3%; Pred. No. 1.5e-26;
 Matches 153; Conservative 105; Mismatches 273; Indels 30; Gaps 11;

QY 6 AEOLITLAEAGVKRYGLVGSLSNPIYDAVROSD-TEVHVHNEEAFAAGAESLITG 64
 DB 28 AOSLRSLSEVADVYFCIGPCTILPAYDPLMDSTVRVRLVYRHEGACAAATGYAQAAG 87
 QY 65 ELAVCAASGPGNTLILQGLVDSHRNGAKVLAISHIPSAQSGTFEGTHPEILKKEES 124
 DB 88 KVGVCATISGPATNLVPIADNLDSPVLVAITGOVSSAIGTDAFQADYVIGTMIT 147
 QY 125 GYCEVNGEGERLILHNAIGSTMACK-GSVVVIIPGDIKEDAGDGTYSNSTISSGTPV 183
 DB 148 KISFLVTKMEDIPRIVIAQFHIASIGRPGVPLVDIKDLKTTSPNRPVMDLPQYRY 207
 QY 184 VERPDEALALVEALINNAKSVTLFCGAGVKMAR--AQVLELAEKIKSPIGHALGKQYIQ 241
 DB 208 TRPAAQIIEAAKLISAARPVLYOCGLAKAKATAEILKVAELTGAPVTTTLMALGAP 267
 QY 242 HENPREVYSGSLGACADNASDADLLLLGTD-----PSSDLPRDNVAQVINDA 295
 DB 268 DSHPLVIGPMGIMGAVTATYALQKADLIVAGARFDRVTGKIDSPAPAKIVHADIDPA 327
 QY 296 HICRTTIVPVTCGVAATIENTILPHVKEKTDSPFLDRMLKAHERKLSVETVY--HN 353

DB 328 EIGKNRAADVPIVGDAREVADLVQAOKKEHDGKND--YSAMKDLISRMDRTYPLIGDQ 386
 QY 354 EKRVPIHPREYASILNELADKDAVFTVDGMCVNHARIENEGRDYVSGRRHGTMAN 413
 DB 387 PEDGSLSPQOVLIERIGQLAPEGTFIAGVGQHQHMAHFVQY-EKDPATVNSGCACTMG 445
 QY 414 ALPHAGASVDRNRQIVAMCGDGLGMLLGLVYKLLHQLPKAVFNNSSLGMYK-LE 472
 DB 446 AVPAAGAAQAGMRGTVMALIDGCGFQMTNQLTTLALNNIPKAVYINNGALGMYRQW 505
 QY 473 MVEGPEREGT-----DHEEVN-----FAEIAAAGIKSVRTDPKRYEQLAEAL 518
 DB 506 TLFYNGRYSNTVLHSGPDVNPPEARCTRVDFVKLSEAMCVCYAIRREDPADLKVIEAN 565
 QY 519 AV-PGVLIDIVDPNALSP 538
 DB 566 SYNDPRVVVDVIEDAMVWP 586

RESULT 15

Q9W218 ID PRELIMINARY: PRT: 584 AA.
 AC 09W218: 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE ACETOLACTATE SYNTHASE, LARGE SUBUNIT.
 GN TM0548.
 OS Thermotoga maritima.
 OC Bacteria; Thermotogales; Thermotoga.
 OX NCBI_Taxid=2336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MSB8 / DSM 3109;
 RA MEDLINE=9287316; PubMed=10360571;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eilen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 RT a genome sequence of Thermotoga maritima.";
 RT Nature 399:323-329(1999).
 CC -1. SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
 DB EMBL: AE001730; AAD35633.1;
 DR HSSP: P06169; 1PVD.
 DR TIGR: TM0548;
 DR INTERPRO: IPR000005;
 DR INTERPRO: IPR000399;
 DR PFAM: PF00205; TTP_enzymes; 1.
 DR PROSITE: PS00041; HTL_ARAQ_FAMILY_1; UNKNOWN_1.
 DR PROSITE: PS00187; TTP_ENZYMES; 1.
 KW Flavoprotein; Lyase; Thiamine pyrophosphate.
 SO SEQUENCE 584 AA: 64431 MW: B2F69CG3D6A4F1205 CRC64;

Query Match 16.8%; Score 502.5; DB 2; Length 584;
 Best Local Similarity 27.1%; Pred. No. 3.4e-26;
 Matches 164; Conservative 103; Mismatches 232; Indels 107; Gaps 21;

QY 6 AEOLITLAEAGVKRYGLVGSLSNPIYDAV--RQSDIEVHNEEAFAAGAESLIT 63
 DB 9 SKMLFEALKEGVDITFGIPGAIINVDDELQNYEDKINIFYLRHQGATHAADGAYRT 68
 QY 64 GELAVCAASGPGNTLILQGLVDSHRNGAKVLAISHIPSAQSGTFEGTHPEILKKEG 123
 DB 69 GRPGVYIVTSGEATFTVYGIAATYMDSTPIYVITGOVFPISGIDAFQEDVDVTGTMPI 128
 QY 124 GYCEVNGEGERLILHNAIQ-----STMAGKSVSVVIIPGDIKEDAGDGTYSNST-I 177
 DB 129 TKHNLVTSIEE---LPRAIKEMFYVATTGRGVPVLLDFPKDIQTAE-GEFNPVPTVEI 183

